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(19) **United States**(12) **Patent Application Publication**
BIELAS(10) **Pub. No.: US 2021/0222243 A1**(43) **Pub. Date: Jul. 22, 2021**(54) **COMPOSITIONS AND METHODS FOR
ACCURATELY IDENTIFYING MUTATIONS**(71) Applicant: **Fred Hutchinson Cancer Research
Center, Seattle, WA (US)**(72) Inventor: **Jason H. BIELAS, Seattle, WA (US)**(21) Appl. No.: **17/219,543**(22) Filed: **Mar. 31, 2021****Related U.S. Application Data**

(60) Continuation of application No. 16/898,155, filed on Jun. 10, 2020, which is a continuation of application No. 16/657,898, filed on Oct. 18, 2019, now abandoned, which is a continuation of application No. 16/121,559, filed on Sep. 4, 2018, now abandoned, which is a continuation of application No. 15/199,784, filed on Jun. 30, 2016, now Pat. No. 10,450,606, which is a division of application No. 14/378,870, filed on Aug. 14, 2014, now Pat. No. 10,011,871, filed as application No. PCT/US2013/026505 on Feb. 15, 2013.

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(57)

ABSTRACT

The present disclosure provides compositions and methods for accurately detecting mutations by uniquely tagging double stranded nucleic acid molecules with dual cyphers such that sequence data obtained from a sense strand can be linked to sequence data obtained from an anti-sense strand when sequenced, for example, by massively parallel sequencing methods.

Specification includes a Sequence Listing.